Egc-cluster Genes Are Lowly Prevalent in Clinical Poultry Staphylococcus Aureus Isolates

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Background & Objectives: Part of *S. aureus* pathogenicity is due to the production of superantigens. Staphylococcal chicken infections are problematic worldwide. The aim of this study was to determine the presence of well-known and more recently described superantigen genes in poultry *S. aureus* isolates.

Methods: Ninety S. aureus that had been collected from tendon sheaths of diseased as well as nose and cloaca of healthy broiler breeders were screened. Isolates were reidentified as S. aureus by colony morphology, standard biochemical tests. PCR amplification of the femA gene was performed to confirm the identification of *S. aureus*. PCR assays were carried out for detecting exfoliative toxins, toxic shock syndrome toxin-1 and 17 staphylococcal enterotoxin genes.

Results: In 22% of the isolates, the egc cluster, containing the enterotoxin genes seg, sei, selm, seln and selo, was found. 18 % and 20 % of isolates were positive for sed and sej, respectively. All isolates were negative for other genes.

Conclusion: Most staphylococcal strains in this study were isolated from lesions contained egc genes cluster. This may be a mere reflection of the difference between clinical isolates and commensal *S. aureus*, as in human S. aureus strains, egc genes cluster are significantly more frequent in commensal strains in comparison with invasive isolates. According to the data represented here, the prevalence of the egc genes cluster in poultry are significantly less frequent in invasive strains in comparison with commensal isolates that have been showed in our previous study.

Keywords: Egc-cluster Genes; Prevalent; Poultry; *Staphylococcus aureus*